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<!--StartFragment-->RESULT 7
Y1610_METJA
ID Y1610_METJA Reviewed; 615 AA.
AC Q59005;
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 26-FEB-2008, entry version 47.
DE Uncharacterized glycosyl hydrolase MJ1610 (EC 3.2.1.-).
GN OrderedLocusNames=MJ1610;
OS Methanocaldococcus jannaschii (Methanococcus jannaschii).
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 15 family.
CC -----
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CC -----
DR EMBL; L77117; AAB99630.1; -; Genomic_DNA.
DR PIR; A64501; A64501.
DR RefSeq; NP_248620.1; -.
DR GeneID; 1452519; -.
DR GenomeReviews; L77117_GR; MJ1610.
DR KEGG; mja:MJ1610; -.
DR TIGR; MJ1610; -.
DR BioCyc; MJAN243232:MJ_1610-MON; -.
DR InterPro; IPR012341; 6hp_glycosidase.
DR InterPro; IPR006465; Glucoamylase.
DR InterPro; IPR000165; Glyco_hydro_15.
DR InterPro; IPR011613; Glyco_hydro_15_rel.
DR Gene3D; G3DSA:1.50.10.10; Cela/Cel48F_cat; 1.
DR Pfam; PF00723; Glyco_hydro_15; 1.
DR TIGRFAMs; TIGR01577; oligosac_amyl; 1.
DR PROSITE; PS00820; GLUCOAMYLASE; 1.
PE 3: Inferred from homology;
KW Complete proteome; Glycosidase; Hydrolase.
FT CHAIN 1 615 Uncharacterized glycosyl hydrolase
FT MJ1610.
FT /FTId=PRO_0000186121.
FT ACT_SITE 403 403 Proton acceptor (By similarity).
FT ACT_SITE 406 406 Proton donor (By similarity).
SQ SEQUENCE 615 AA; 72008 MW; 2B37EB89F0357BE5 CRC64;

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Query Match 55.0%; Score 1841.5; DB 1; Length 615;
 Best Local Similarity 51.5%; Pred. No. 3e-113;
 Matches 320; Conservative 143; Mismatches 149; Indels 9; Gaps 5;

Qy	1	MAGIIGNGNLLAKIDDLGSIEYIFFPHLGYETHILDTSFaiYYNNKIKWHWDHSWDVSNQ	60
Db	4	MGGIVGNNSLLAKIGDYGIEYLFYPQVGYETHFFDSALAV-YDKKVKWHWDDDDWDITQK	62
Qy	61	YLKDSNILKTTYENDDFLIYSKDCVSIshNLIVKQLSIINKTNSEKDIKFFFYENLRIGE	120
Db	63	YIEETNIFKTILEDKIIILTikDFVPVSHNVLIrrVYIKNKLdKKLNfKLFfFYENLRIGE	122
Qy	121	TPSKSTVkfVKEKNCLIKHDkNYIFCIGSNKKVSSYQCGIKYSESSALRDIENGVLKEQS	180
Db	123	NPITNTVKfL-EDGCIVkYNGkYIFCIGSDKRIDSfQCGNRYSKTSAYIDIENGILKEHK	181
Qy	181	SATGLITDSALCWEfKIKPNQKYtLSILILPEKYDGDYNKtLNlMDtLHMVKDNLdKLYN	240
Db	182	ESSGLLTDSAISWNiKIDEKRSLaFNiYILPQRfDGDfS---IITEQLKIIMNNSENiKN	238
Qy	241	LTRNfWKSRVDSMVNKWGILKLEeYKECIDICKRSLlTLLlLCDYKGGIIASPSLHPDYR	300
Db	239	LSMNYWK-HIIGEINRFiHPELRQNnKIYSITKRAlMTLLmLCDKEGGIIAAPSfLHPDYR	297
Qy	301	YVWCRDAGYMAVALDLCGQHemSEKYfEWCKTTQNSDGSWVQNYyVEGYPRfTAiQIDQV	360
Db	298	YVWGRDGSYISIALDLFGIRNIPDRfFEfFMSKiQnADGSWLQNYyVNGKPRLTaiQTDQI	357
Qy	361	GTTIWALLVHYRITGDKHfLKRnWEMVKKAGDYLSRAADQLIPCYDLWEEKfGVfAYTLG	420
Db	358	GSILWAMDVHYRLTGDRKfVERYWNTIEKAANYLRLVALNfTPCFDLWEERfGVfAYTMG	417
Qy	421	AIYGGfLKSgYLiGkELDKEEEIQHWKKSMMnFLKNEVvNRlyLKNEKRfAKSLKPLDKTID	480
Db	418	ATYAGfLKcAYSMSKAVNKRdKVdWGKTIEfLKHEVPKRfYLEDEERfAKSiNPLDKTID	477
Qy	481	TSILGLSFpyGLVSVDDPRIISTANQIEKAFNYKVGgVGRYPEDIYfGGNPWiITTLWLY	540
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Qy	541	MYYKKLVDTLSKKGKfQESiIDNynKKCYNLLKWiLKHQFNGMfPEQVHKDLGiPiSAIP	600
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Qy	601	LGWSHAMVIAIHGDYDILIP	621
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<!--EndFragment-->